

## SEQUENCE LISTING

&lt;110&gt; Delagrave, Simon

&lt;120&gt; BIOTHERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS

&lt;130&gt; BTS 0002-500

&lt;160&gt; 28

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&lt;210&gt; 1

&lt;211&gt; 354

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; hCASK-PDZopt

&lt;400&gt; 1

tttttatgcg gccagccgg ccggatccgg tatggatatg gaaaatgtta cccgtgttcg 60

tttagttcaa tttcaaaaaa ataccgatga accaatgggt attaccttga aaatgaatga 120

attgaatcat tgtattgttg cccgtattat gcatgggtgg atgattcatc gtcaagggtac 180

tttgcattgtt ggtgatgaaa ttcgtgaaat taatgggtatt tctgttgcca atcaaaccgt 240

tgaacaattg caaaaaatgt tgcgtgaaat gcgtgggttct attaccttta aaattgttcc 300

atcttatcgt acccaatctt cttctggaat tcatgcggcc gctgggtgctc cagt 354

&lt;210&gt; 2

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; hCask-PDZopt

&lt;400&gt; 2

Gly Met Asp Met Glu Asn Val Thr Arg Val Arg Leu Val Gln Phe Gln  
1 5 10 15Lys Asn Thr Asp Glu Pro Met Gly Ile Thr Leu Lys Met Asn Glu Leu  
20 25 30Asn His Cys Ile Val Ala Arg Ile Met His Gly Gly Met Ile His Arg  
35 40 45Gln Gly Thr Leu His Val Gly Asp Glu Ile Arg Glu Ile Asn Gly Ile  
50 55 60Ser Val Ala Asn Gln Thr Val Glu Gln Leu Gln Lys Met Leu Arg Glu  
65 70 75 80

Met Arg Gly Ser Ile Thr Phe Lys Ile Val Pro Ser Tyr Arg Thr Gln  
                             85                            90                            95

Ser Ser Ser

<210> 3  
 <211> 337  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> hCASK-PDZ-GST fusion  
 <400> 3

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
  1                            5                            10                            15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
                             20                            25                            30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
                             35                            40                            45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
                             50                            55                            60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
  65                            70                            75                            80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
                             85                            90                            95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
                             100                            105                            110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
                             115                            120                            125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
                             130                            135                            140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
  145                            150                            155                            160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
                             165                            170                            175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
                             180                            185                            190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Arg Arg Ala Ser Val Gly Ser Gly Met Asp Met Glu Asn Val  
 225 230 235 240  
 Thr Arg Val Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met  
 245 250 255  
 Gly Ile Thr Leu Lys Met Asn Glu Leu Asn His Cys Ile Val Ala Arg  
 260 265 270  
 Ile Met His Gly Gly Met Ile His Arg Gln Gly Thr Leu His Val Gly  
 275 280 285  
 Asp Glu Ile Arg Glu Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val  
 290 295 300  
 Glu Gln Leu Gln Lys Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe  
 305 310 315 320  
 Lys Ile Val Pro Ser Tyr Arg Thr Gln Ser Ser Ser Gly Ile His Arg  
 325 330 335

Asp

<210> 4  
 <211> 590  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> hCASK-PDZ-alkaline phosphatase fusion

<400> 4

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala  
 1 5 10 15  
 Phe Cys Leu Pro Val Phe Ala Gly Met Asp Met Glu Asn Val Thr Arg  
 20 25 30  
 Val Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met Gly Ile  
 35 40 45

Thr Leu Lys Met Asn Glu Leu Asn His Cys Ile Val Ala Arg Ile Met  
 50 55 60  
 His Gly Gly Met Ile His Arg Gln Gly Thr Leu His Val Gly Asp Glu  
 65 70 75 80  
 Ile Arg Glu Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val Glu Gln  
 85 90 95  
 Leu Gln Lys Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe Lys Ile  
 100 105 110  
 Val Pro Ser Tyr Arg Thr Gln Ser Ser Ser Arg Thr Pro Glu Met Pro  
 115 120 125  
 Leu Gln Gly Thr Ala Val Asp Gly Gly Gly Gly Ser Met His Ala Ser  
 130 135 140  
 Leu Glu Val Leu Glu Asn Arg Ala Ala Gln Gly Asp Ile Thr Ala Pro  
 145 150 155 160  
 Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala Ala Leu Arg Asp  
 165 170 175  
 Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu Leu Ile Gly Asp  
 180 185 190  
 Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn Tyr Ala Glu Gly  
 195 200 205  
 Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro Leu Thr Gly Gln  
 210 215 220  
 Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys Pro Asp Tyr Val  
 225 230 235 240  
 Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr Gly Val Lys Thr  
 245 250 255  
 Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys Asp His Pro Thr  
 260 265 270  
 Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser  
 275 280 285  
 Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu Val Ala His Val  
 290 295 300

Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro  
 305 310 315 320  
 Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile Thr Glu Gln Leu  
 325 330 335  
 Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly Ala Lys Thr Phe  
 340 345 350  
 Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg Glu  
 355 360 365  
 Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu  
 370 375 380  
 Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe  
 385 390 395 400  
 Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro Lys Ala Thr Tyr  
 405 410 415  
 His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr Pro Asn Pro Gln  
 420 425 430  
 Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr Asp Lys Ala Ile  
 435 440 445  
 Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu Gln Val Glu Gly  
 450 455 460  
 Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro Cys Gly Gln Ile  
 465 470 475 480  
 Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg Ala Leu Glu Phe  
 485 490 495  
 Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr Ala Asp His Ala  
 500 505 510  
 His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr  
 515 520 525  
 Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly  
 530 535 540  
 Asn Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile  
 545 550 555 560

Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly Leu Thr Asp Gln  
565 570 575

Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly Leu Lys  
580 585 590

<210> 5  
<211> 351  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> hCASK-PDZ-fc fusion protein

<400> 5

Met Arg Ala Pro Ala Gln Ile Phe Gly Phe Leu Leu Leu Leu Phe Pro  
1 5 10 15

Gly Thr Arg Cys Gly Met Asp Met Glu Asn Val Thr Arg Val Arg Leu  
20 25 30

Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met Gly Ile Thr Leu Lys  
35 40 45

Met Asn Glu Leu Asn His Cys Ile Val Ala Arg Ile Met His Gly Gly  
50 55 60

Met Ile His Arg Gln Gly Thr Leu His Val Gly Asp Glu Ile Arg Glu  
65 70 75 80

Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val Glu Gln Leu Gln Lys  
85 90 95

Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe Lys Ile Val Pro Ser  
100 105 110

Tyr Arg Thr Gln Ser Ser Ser Glu Pro Lys Ser Cys Asp Lys Thr His  
115 120 125

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val  
130 135 140

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
145 150 155 160

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu  
165 170 175

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
180 185 190

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser  
195 200 205

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Asp Tyr Lys  
210 215 220

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Met Gln Lys Thr Ile  
225 230 235 240

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro  
245 250 255

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu  
260 265 270

Val Lys Gly Phe Tyr Pro Arg His Ile Ala Val Glu Trp Glu Ser Asn  
275 280 285

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
290 295 300

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg  
305 310 315 320

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
325 330 335

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
340 345 350

<210> 6  
<211> 128  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> polyhistidine tagged and secreted hCASK-PDZ

<400> 6

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala  
1 5 10 15

Phe Cys Leu Pro Val Phe Ala Gly Met Asp Met Glu Asn Val Thr Arg  
20 25 30

Val Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met Gly Ile  
35 40 45

Thr Leu Lys Met Asn Glu Leu Asn His Cys Ile Val Ala Arg Ile Met  
50 55 60

His Gly Gly Met Ile His Arg Gln Gly Thr Leu His Val Gly Asp Glu  
65 70 75 80

Ile Arg Glu Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val Glu Gln  
85 90 95

Leu Gln Lys Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe Lys Ile  
100 105 110

Val Pro Ser Tyr Arg Thr Gln Ser Ser Ser His His His His His His  
115 120 125

<210> 7  
<211> 122  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> secreted hCASK-PDZ

<400> 7

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala  
1 5 10 15

Phe Cys Leu Pro Val Phe Ala Gly Met Asp Met Glu Asn Val Thr Arg  
20 25 30

Val Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met Gly Ile  
35 40 45

Thr Leu Lys Met Asn Glu Leu Asn His Cys Ile Val Ala Arg Ile Met  
50 55 60

His Gly Gly Met Ile His Arg Gln Gly Thr Leu His Val Gly Asp Glu  
65 70 75 80

Ile Arg Glu Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val Glu Gln  
85 90 95

Leu Gln Lys Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe Lys Ile  
100 105 110

Val Pro Ser Tyr Arg Thr Gln Ser Ser Ser  
115 120

<210> 8  
<211> 234



&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; NHERF PDZ dimer

&lt;400&gt; 8

Pro Arg Leu Cys Cys Leu Glu Lys Gly Pro Asn Gly Tyr Gly Phe His  
 1 5 10 15

Leu His Gly Glu Lys Gly Lys Leu Gly Gln Tyr Ile Arg Leu Val Glu  
 20 25 30

Pro Gly Ser Pro Ala Glu Lys Ala Gly Leu Leu Ala Gly Asp Arg Leu  
 35 40 45

Val Glu Val Asn Gly Glu Asn Val Glu Lys Glu Thr His Gln Gln Val  
 50 55 60

Val Ser Arg Ile Arg Ala Ala Leu Asn Ala Val Arg Leu Leu Val Val  
 65 70 75 80

Asp Pro Glu Thr Asp Glu Gln Leu Gln Lys Leu Gly Val Gln Val Arg  
 85 90 95

Glu Glu Leu Leu Arg Ala Gln Glu Ala Pro Gly Gln Ala Glu Pro Pro  
 100 105 110

Ala Ala Ala Glu Val Gln Gly Ala Gly Asn Glu Asn Glu Pro Arg Glu  
 115 120 125

Ala Asp Lys Ser His Pro Glu Gln Arg Glu Leu Arg Pro Arg Leu Cys  
 130 135 140

Thr Met Lys Lys Gly Pro Ser Gly Tyr Gly Phe Asn Leu His Ser Asp  
 145 150 155 160

Lys Ser Lys Pro Gly Gln Phe Ile Arg Ser Val Asp Pro Asp Ser Pro  
 165 170 175

Ala Glu Ala Ser Gly Leu Arg Ala Gln Asp Arg Ile Val Glu Val Asn  
 180 185 190

Gly Val Cys Met Glu Gly Lys Gln His Gly Asp Val Val Ser Ala Ile  
 195 200 205

Arg Ala Gly Gly Asp Glu Thr Lys Leu Leu Val Val Asp Arg Glu Thr  
 210 215 220

Asp Glu Phe Phe Lys Lys Cys Arg Val Ile  
225 230

<210> 9  
<211> 546  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> third PDZ domain of human Dlg1

<400> 9

Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ala  
1 5 10 15

Ala Gln Pro Ala Ala Val Leu Gly Asp Asp Glu Ile Thr Arg Glu Pro  
20 25 30

Arg Lys Val Val Leu His Arg Gly Ser Thr Gly Leu Gly Phe Asn Ile  
35 40 45

Val Gly Gly Glu Asp Gly Glu Gly Ile Phe Ile Ser Phe Ile Leu Ala  
50 55 60

Gly Gly Pro Ala Asp Leu Ser Gly Glu Leu Arg Lys Gly Asp Arg Ile  
65 70 75 80

Ile Ser Val Asn Ser Val Asp Leu Arg Ala Ala Ser His Glu Gln Ala  
85 90 95

Ala Ala Ala Leu Lys Asn Ala Gly Gln Ala Val Thr Ile Val Ala Gln  
100 105 110

Tyr Arg Pro Glu Glu Tyr Ser Arg Phe Glu Ala Ala Ala Ala Gly Ala  
115 120 125

Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg Ala Ala Gln Thr Val  
130 135 140

Glu Ser Cys Leu Ala Lys Pro His Thr Glu Asn Ser Phe Thr Asn Val  
145 150 155 160

Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys  
165 170 175

Leu Trp Asn Ala Thr Gly Val Val Val Cys Thr Gly Asp Glu Thr Gln  
180 185 190

Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu Ala Ile Pro Glu Asn Glu  
195 200 205

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly  
 210 215 220  
 Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr  
 225 230 235 240  
 Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln  
 245 250 255  
 Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn  
 260 265 270  
 Thr Phe Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu  
 275 280 285  
 Thr Val Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr  
 290 295 300  
 Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr  
 305 310 315 320  
 Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu  
 325 330 335  
 Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln  
 340 345 350  
 Pro Pro Val Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
 355 360 365  
 Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser  
 370 375 380  
 Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr  
 385 390 395 400  
 Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp  
 405 410 415  
 Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala  
 420 425 430  
 Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly  
 435 440 445  
 Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser  
 450 455 460

Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn  
465 470 475 480

Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro  
485 490 495

Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp  
500 505 510

Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala  
515 520 525

Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys  
530 535 540

Glu Ser  
545

<210> 10  
<211> 485  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> third PDZ domain of human Dlg1

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ggagatgatg aaattacaag ggaacctaga aaagttgttc ttcacgtgg ctcaacgggc 120  
cttggtttca acattgtagg aggagaagat ggagaaggaa tatttatttc ctttatctta 180  
gccggaggac ctgctgatct aagtggagag ctcagaaaag gagatcgat tatatcggtta 240  
aacagtgttg acctcagagc tgctagtcac gagcaggcag cagctgcatt gaaaaatgct 300  
ggccaggctg tcacaattgt tgcacaatat cgacctgaag aatacagtcg ttttgaagct 360  
gcggccgcag gtgcgccggt gccgtatccg gatccgctgg aaccgcgtgc cgcatagact 420  
gttgaaagtt gtttagcaaa acctcataca gaaaattcat ttactaacgt ctggaaagac 480  
gacaa 485

<210> 11  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> HA peptide

<400> 11

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala  
1 5

<210> 12  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Tat protein

<400> 12

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
1 5 10

<210> 13  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> hCASK ligand

<400> 13

Gln Lys Ala Pro Thr Lys Glu Phe Tyr Ala  
1 5 10

<210> 14  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> pCAN5' primer

<400> 14  
catgattacg ccaagctttg g

21

<210> 15  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> pCAN3' primer

<400> 15  
cgatctaaag ttttgtcgtc

20

<210> 16  
<211> 59  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> NNK1B

<220>  
 <221> misc\_feature  
 <222> (25)..(26)  
 <223> n is a, c, g, or t

<220>  
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 <222> (31)..(32)  
 <223> n is a, c, g, or t

<220>  
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 <222> (37)..(38)  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (24)..(30)  
 <223> m is a or c

<220>  
 <221> misc\_feature  
 <222> (36)..(36)  
 <223> m is a or c

<400> 16  
 caatgattca attcattcat tttmnnnggtm nnaccmnntg gttcatcggt attttttttg 59

<210> 17  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> NNK2A

<400> 17  
 aaaatgaatg aattgaatca ttg 23

<210> 18  
 <211> 59  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> NNK2B

<220>  
 <221> misc\_feature  
 <222> (23)..(24)  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (26)..(27)  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (35)..(36)

<223> n is a, c, g, or t

<220>

<221> misc\_feature

<222> (22)..(25)

<223> m is a or c

<220>

<221> misc\_feature

<222> (24)..(24)

<223> m is a or c

<400> 18

ggtaatagaa ccacgcattt cmnmnnncat tttmnncaat tgttcaacgg tttgattgg 59

<210> 19

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> NNK3A

<400> 19

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<210> 20

<211> 489

<212> DNA

<213> Artificial Sequence

<220>

<223> hCASK PDZ

<220>

<221> misc\_feature

<222> (179)..(180)

<223> n is a, c, g, or t

<220>

<221> misc\_feature

<222> (185)..(186)

<223> n is a, c, g, or t

<220>

<221> misc\_feature

<222> (191)..(192)

<223> n is a, c, g, or t

<220>

<221> misc\_feature

<222> (335)..(336)

<223> n is a, c, g, or t

<220>

<221> misc\_feature

<222> (344)..(345)

<223> n is a, c, g, or t

<220>

<221> misc\_feature

<222> (347)..(348)  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (181)..(187)  
 <223> k is g or t

<220>  
 <221> misc\_feature  
 <222> (193)..(193)  
 <223> k is g or t

<220>  
 <221> misc\_feature  
 <222> (337)..(337)  
 <223> k is g or t

<220>  
 <221> misc\_feature  
 <222> (346)..(349)  
 <223> k is g or t

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 attcgcaatt ccttttagttg ttcttttcta tgcggcccgag ccggccggat ccggtatgga 120  
 tatggaaaat gttaccctgtg ttcgtttagt tcaatttcaa aaaaataccg atgaaccann 180  
 kggtnnkacc nnkaaatga atgaattgaa tcattgtatt gttgcccgta ttatgcatgg 240  
 tggatgatt catcgtcaag gtactttgca tgttggtgat gaaattcgtg aaattaatgg 300  
 tatttctgtt gccaatcaaa ccggtgaaca attgnnkaaa atgnnknnkg aaatgcgtgg 360  
 ttctattacc tttaaaattg ttccatctta tcgtacccaa tcttcttctg gaattcatgc 420  
 ggccgcaggt gcgccggtgc cgtatccgga tccgctggaa ccgcgtgccg catagactgt 480  
 tgaaagttg 489

<210> 21  
 <211> 59  
 <212> DNA  
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<220>  
 <223> TSM1B

<220>  
 <221> misc\_feature  
 <222> (32)..(32)  
 <223> b is c, g or t

<220>  
 <221> misc\_feature  
 <222> (38)..(38)  
 <223> k is g or t

<220>  
 <221> misc\_feature  
 <222> (26)..(26)



<223> n is a, c, g, or t

<220>

<221> misc\_feature

<222> (31)..(31)

<223> r is a or g

<400> 21

caatgattca attcattcat ttttaanggta rbacccaktg gttcatcggt attttttttg 59

<210> 22

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> TSM2A

<400> 22

aaaatgaatg aattgaatca ttg 23

<210> 23

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> TSM2B

<220>

<221> misc\_feature

<222> (27)..(27)

<223> k is g or t

<220>

<221> misc\_feature

<222> (36)..(36)

<223> k is g or t

<220>

<221> misc\_feature

<222> (22)..(25)

<223> m is a or c

<220>

<221> misc\_feature

<222> (34)..(34)

<223> m is a or c

<220>

<221> misc\_feature

<222> (35)..(35)

<223> w is a or t

<220>

<221> misc\_feature

<222> (23)..(23)

<223> y is c or t

<400> 23

ggtaatagaa ccacgcattt cmytmakcat tttmwkcaat tgttcaacgg tttgattgg 59

<210> 24  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> TSM3A

<400> 24  
gaaatgcgtg gttctattac c

21

<210> 25  
<211> 489  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> hCASK PDZ

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<222> (186)..(186)

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tatggaaaat gttaccctgtg ttcgttttagt tcaatttcaa aaaaataccg atgaaccamt      180
gggtvytacc nttaaaatga atgaattgaa tcattgtatt gttgcccgtg ttatgcatgg      240
tggtatgatt catcgtcaag gtactttgca tgttggtgat gaaattcgtg aaattaatgg      300
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ttctattacc tttaaaattg ttccatctta tcgtacccaa tcttcttctg gaattcatgc      420
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<213> Artificial Sequence

<220>

<223> C-terminus of BclA

<400> 26

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<210> 27

<211> 12

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<223> Control peptide

<400> 27

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His Arg Arg Ser Ala Arg Tyr Leu Asp Thr Val Leu
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<210> 28

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<223> peptide ligand of the third PDZ domain of human Dlg1

<400> 28

Ser Ser Leu Gln Ser Leu Glu Thr Ser Val  
1 5 10